

WHAT IS CLAIMED IS:

1. An isolated or recombinant polypeptide:
 - A) that:
 - 5 a) specifically binds polyclonal antibodies generated against a 12 consecutive amino acid segment of SEQ ID NO: 2; and
 - b) comprises at least one sequence selected from the following group (see SEQ ID NO: 2):
 - 10 LeuCysPheArgMetLysAsp; ValLeuTyrLeuHisAsn;
GlnLeuLeuAlaGly; IleSerValValProAsn;
SerProValIleLeuGlyVal; GlnCysLeuSerCysGlyThr;
ProIleLeuLysLeuGlu; PheTyrArgArgAspMetGly;
LeuThrSerSerPheGluSer; PheLeuCysThrSer;
15 GlnProValArgLeuThr; PheTyrPheGlnGln;
ArgAlaLeuAspAlaSerLeu; and GlyLeuHisAlaGluLysVal;
 - B) that:
 - 20 a) specifically binds polyclonal antibodies generated against a 12 consecutive amino acid segment of SEQ ID NO: 6; and
 - b) comprises at least one sequence selected from the following group (see SEQ ID NO: 6):
 - 25 SerLeuArgHisValGlnAsp; ValTrpIleLeuGlnAsn;
IleLeuThrAlaVal; IleThrLeuLeuProCys;
AspProThrTyrMetGlyVal; SerCysLeuPheCysThrLys;
ProValLeuGlnLeuGly; PheTyrHisLysLysSerGly;
ThrThrSerThrPheGluSer; PheIleAlaValCys;
CysProLeuIleLeuThr; PheGluMetIleVal;
GlnAspLeuSer; ValProArgLysGluGlnThrVal;
30 SerLysGlySerCysPro; ArgAlaAlaSer;
ProCysGlnTyrLeuAspThrLeuGlu; and SerGlyThrThr; or
 - C) that:
 - 35 a) specifically binds polyclonal antibodies generated against a 12 consecutive amino acid segment of SEQ ID NO: 13 or 15; and
 - b) comprises at least one sequence selected from the following group (see SEQ ID NO: 13 or 15):

ITGTIND; VWTLQG; NLVAV; VAVITC; DPIYLG I; MCLYCEK;
PTLQLK; FYRAKTG; RTSTLES; FIASS; QPIILT; FELNI;
SMCK; NDLN; VPR(R/S)TSVT; VPRSDSVT; TCKYPEALE;
TGRT; SKRDQP; or SKGDQP.

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2. The polypeptide of Claim 1:

- a) wherein said polypeptide comprises a plurality of
said sequences selected from said group in
section b) of part 1A;
- 10 b) wherein said polypeptide comprises a plurality of
said sequences selected from said group in
section b) of part 1B;
- c) wherein said polypeptide comprises a plurality of
said sequences selected from said group in
15 section b) of part 1C; or
- d) which specifically binds to polyclonal antibodies
generated against an immunogen selected from the
group consisting of:
- i) the polypeptide of SEQ ID NO: 2;
- 20 ii) the polypeptide of SEQ ID NO: 6;
- iii) the polypeptide of SEQ ID NO: 13; and.
- iv) the polypeptide of SEQ ID NO: 15.

3. The polypeptide of:

- 25 A) Claim 1A, wherein said 12 consecutive amino acid
segment is selected from (see SEQ ID NO: 2):
LeuCysPheArgMetLysAspSerAlaLeuLysValLeuTyrLeuHisAsn-
Asn;
IleSerValValProAsnArgAlaLeuAspAlaSerLeuSerProValIle-
30 LeuGlyValGln;
SerProValIleLeuGlyValGlnGlyGlySerGlnCys;
ProIleLeuLysLeuGluProValAsnIleMetGluLeu;
ThrSerSerPheGluSerAlaAlaTyrProGlyTrpPhe;
PheLeuCysThrSerProGluAlaAspGlnProVal;
35 ThrGlnIleProGluAspProAlaTrpAspAlaProIle; or
ThrSerSerPheGluSerAlaAlaTyrProGlyTrpPhe;

- B) Claim 1B, wherein said 12 consecutive amino acid segment is selected from (see SEQ ID NO: 6):
ArgAlaAlaSerProSerLeuArgHisValGlnAspLeu;
SerSerArgValTrpIleLeuGlnAsnAsnIleLeu;
5 ProValThrIleThrLeuLeuProCysGlnTyrLeu;
GlyValGlnArgProMetSerCysLeuPheCysThr;
PheCysThrLysAspGlyGluGlnProValLeuGlnLeu;
ThrSerThrPheGluSerAlaAlaPheProGlyTrpPhe; and
CysSerLysGlySerCysProLeuIleLeuThrGln; or
- 10 C) claim 1C, wherein said 12 consecutive amino acid segment is selected from (see SEQ ID NO: 13 or 15):
SMCKPITGTINDL;
NQQVWTLQGQNL;
PVTVAVITCKYP;
15 GIGNPEMCLYCE;
YCEKVGEQPTLQL;
TSTLESVAFPDWF;
SKGDQPIILTSE;
SKRDQPIILTSE; and
20 GKSNTAFELNIND.

3. The polypeptide of Claim 2, wherein said polypeptide:

- 25 i) is a mature protein;
ii) lacks a post-translational modification;
iii) is from a rodent, including a mouse;
iv) is from a primate, including a human;
v) is a natural allelic variant of IL-1 δ or IL-1 ϵ ;
vi) has a length at least 30 amino acids;
30 vii) exhibits at least two non-overlapping epitopes that are specific for a rodent IL-1 δ ;
viii) exhibits a sequence identity over a length of at least about 20 amino acids to SEQ ID NO: 2;
ix) exhibits at least two non-overlapping epitopes
35 which are specific for a rodent or primate IL-1 ϵ ;
x) exhibits a sequence identity over a length of at least about 20 amino acids to SEQ ID NO: 6 or 15;

- xi) is glycosylated;
xii) has a molecular weight of at least 10 kD with
natural glycosylation;
xiii) is a synthetic polypeptide;
5 xiv) is attached to a solid substrate;
xv) is conjugated to another chemical moiety;
xvi) is a 5-fold or less substitution from natural
sequence; or
xvii) is a deletion or insertion variant from a
10 natural sequence.
4. A soluble polypeptide comprising:
a) a sterile polypeptide of Claim 2;
b) said sterile polypeptide of Claim 2 and a carrier,
15 wherein said carrier is:
i) an aqueous compound, including water, saline,
and/or buffer; and/or
ii) formulated for oral, rectal, nasal, topical,
or parenteral administration.
20
5. A fusion protein having a polypeptide sequence of
Claim 2 and further comprising:
a) a mature protein of Claim 2;
b) a detection or purification tag, including a FLAG,
25 His6, or Ig sequence; or
c) sequence of another cytokine or chemokine.
6. A kit comprising a polypeptide of Claim 2, and:
a) a compartment comprising said protein or
30 polypeptide; and/or
b) instructions for use or disposal of reagents in
said kit.
7. A binding compound comprising an antigen binding
35 site from an antibody, which specifically binds to a mature
polypeptide from:
a) SEQ ID NO: 2;

- b) SEQ ID NO: 6;
- c) SEQ ID NO: 13; or
- d) SEQ ID NO: 15.

5 8. The binding compound of Claim 7, wherein:

- a) said binding compound is an Fv, Fab, or Fab2 fragment;
- b) said binding compound is conjugated to another chemical moiety; or
- 10 c) said antibody:
 - i) is raised against a polypeptide comprising a 12 consecutive amino acid segment of SEQ ID NO: 2, 6, 13, or 15;
 - ii) is raised against a mature IL-1 ϵ ;
 - 15 iii) is raised to a purified rodent IL-1 δ or rodent or primate IL-1 ϵ ;
 - iv) is immunoselected;
 - v) is a polyclonal antibody;
 - vi) binds to a denatured IL-1 δ or IL-1 ϵ ;
 - 20 vii) exhibits a K_d to antigen of at least 30 μ M;
 - viii) is attached to a solid substrate, including a bead or plastic membrane;
 - ix) is in a sterile composition; or
 - x) is detectably labeled, including a
 - 25 radioactive or fluorescent label.

9. A kit comprising said binding compound of Claim 7, and:

- a) a compartment comprising said binding compound; and/or
- 30 b) instructions for use or disposal of reagents in said kit.

10. A composition comprising:

- 35 a) a sterile binding compound of Claim 7, or
- b) said binding compound of Claim 7 and a carrier, wherein said carrier is:

- i) an aqueous compound, including water, saline, and/or buffer; and/or
- ii) formulated for oral, rectal, nasal, topical, or parenteral administration.

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11. An isolated or recombinant nucleic acid encoding a polypeptide of Claim 2, wherein:

- a) said polypeptide of Claim 2 is IL-1 δ or IL-1 ϵ from a mammal; or
- 10 b) said nucleic acid:
 - i) comprises the mature coding sequence of SEQ ID NO: 1, 3, 12, or 14;
 - ii) encodes an antigenic peptide sequence of SEQ ID NO: 2, or SEQ ID NO: 6, 13, or 15;
 - 15 iii) encodes a plurality of antigenic peptide sequences of SEQ ID NO: 2, or SEQ ID NO: 6, 13, or 15;
 - iv) exhibits identity to a natural cDNA encoding said segment;
 - 20 v) is an expression vector;
 - vi) further comprises an origin of replication;
 - vii) is from a natural source;
 - viii) comprises a detectable label;
 - ix) comprises synthetic nucleotide sequence;
 - 25 x) is less than 6 kb, preferably less than 3 kb;
 - xi) is from a rodent or primate;
 - xii) comprises a natural full length coding sequence;
 - xiii) is a hybridization probe for a gene
 - 30 encoding said IL-1 δ or IL-1 ϵ ;
 - xiv) is a PCR primer, PCR product, or mutagenesis primer; or
 - xv) encodes an IL-1 δ or an IL-1 ϵ protein.

35 12. A cell, transformed with said nucleic acid of Claim 10.

13. The cell of Claim 12, wherein said cell is:
- a) a prokaryotic cell;
 - b) a eukaryotic cell;
 - c) a bacterial cell;
 - 5 d) a yeast cell;
 - e) an insect cell;
 - f) a mammalian cell;
 - g) a murine cell;
 - h) a primate cell; or
 - 10 i) a human cell.
14. A kit comprising said nucleic acid of Claim 11, and:
- a) a compartment comprising said nucleic acid;
 - 15 b) a compartment further comprising a mammalian IL-1 δ or IL-1 ϵ protein or polypeptide; and/or
 - c) instructions for use or disposal of reagents in said kit.
- 20 15. An isolated or recombinant nucleic acid that
- a) hybridizes under wash conditions of 40° C and less than 1M salt to SEQ ID NO: 1;
 - b) hybridizes under wash conditions of 40° C and less than 1 M salt to SEQ ID NO: 3, 5, 12 or 14.
- 25 16. The nucleic acid of Claim 15, wherein:
- a) said wash condition is at 50° C and/or 500 mM salt; and
 - b) exhibits identity over at least 20 nucleotides to
 - 30 SEQ ID NO: 1, 3, 5, 12, or 14.
17. The nucleic acid of Claim 16, wherein:
- a) a wash condition is at 65° C and/or 150 mM salt; or
 - 35 b) exhibits identity over at least 50 nucleotides to SEQ ID NO: 1, 3, 5, 12, or 14.

18. A method of modulating a cell involved in an inflammatory response comprising contacting said cell with an agonist or antagonist of a mammalian IL-1 δ or IL-1 ϵ polypeptide of Claims 1.

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19. The method of Claim 18, wherein:

- a) said contacting is in combination with an agonist or antagonist of IL-1 α , IL-1RA, IL-1 β , IL-1 γ , IL-2, and/or IL-12;
- 10 b) said contacting is with an antagonist, including binding composition comprising an antibody binding site which specifically binds an IL-1 δ or IL-1 ϵ ; or
- c) said modulating is regulation of IFN- γ production.

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20. A method of:

- A) making an antiserum comprising an antibody of Claim 7, comprising immunizing a mammal with an immunogenic amount of:
 - 20 a) a rodent IL-1 δ polypeptide;
 - b) a peptide sequence comprising a 12 consecutive amino acid segment of SEQ ID NO: 2;
 - c) a rodent or primate IL-1 ϵ polypeptide; or
 - 25 d) a peptide sequence comprising a 12 consecutive amino acid segment of SEQ ID NO: 6, 13, or 15;thereby causing said antiserum to be produced; or
- B) producing an antigen:antibody complex, comprising
 - 30 contacting:
 - a) a rodent IL-1 δ protein or peptide with an antibody of Claim 7; or
 - b) a rodent or primate IL-1 ϵ protein or peptide with an antibody of Claim 7;
 - 35 thereby allowing said complex to form.

SEQUENCE SUBMISSION

SEQ ID NO: 1 provides rodent IL-1 δ nucleotide sequence.
SEQ ID NO: 2 provides rodent IL-1 δ polypeptide sequence.
5 SEQ ID NO: 3 provides partial rodent IL-1 ϵ nucleotide sequence.
SEQ ID NO: 4 provides partial rodent IL-1 ϵ polypeptide sequence.
SEQ ID NO: 5 provides full length rodent IL-1 ϵ nucleic acid sequence.
SEQ ID NO: 6 provides full length rodent IL-1 ϵ polypeptide sequence.
SEQ ID NO: 7 provides human IL-1RA precursor polypeptide sequence.
10 SEQ ID NO: 8 provides human IL-1 γ (IGIF) precursor polypeptide sequence.
SEQ ID NO: 9 provides mouse IL-1 γ (IGIF) precursor polypeptide sequence.
SEQ ID NO: 10 provides human IL-1 α precursor polypeptide sequence.
SEQ ID NO: 11 provides human IL-1 α precursor polypeptide sequence.
SEQ ID NO: 12 provides primate IL-1 ϵ nucleotide sequence.
15 SEQ ID NO: 13 provides primate IL-1 ϵ polypeptide sequence.
SEQ ID NO: 14 provides full length primate IL-1 ϵ nucleic acid sequence.
SEQ ID NO: 15 provides full length primate IL-1 ϵ polypeptide sequence.

20 (1) GENERAL INFORMATION:

(i) APPLICANT: Hedrick, Joseph A.
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(ii) TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
and Methods

30 (iii) NUMBER OF SEQUENCES: 15

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(E) COUNTRY: USA
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40 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
45 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 470 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

30 (A) NAME/KEY: CDS

(B) LOCATION: 1..468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

35	ATG ATG GTT CTG AGT GGG GCA CTA TGC TTC CGA ATG AAG GAT TCA GCC	48
	Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala	
	1 5 10 15	
40	TTG AAG GTA CTG TAT CTG CAC AAT AAC CAG CTG CTG GCT GGA GGA CTG	96
	Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu	
	20 25 30	
45	CAC GCA GAG AAG GTC ATT AAA GGT GAG GAG ATC AGT GTT GTC CCA AAT	144
	His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn	
	35 40 45	
50	CGG GCA CTG GAT GCC AGT CTG TCC CCT GTC ATC CTG GGC GTT CAA GGA	192
	Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly	
	50 55 60	
55	GGA AGC CAG TGC CTA TCT TGT GGG ACA GAG AAA GGG CCA ATT CTG AAA	240
	Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys	
	65 70 75 80	
60	CTT GAG CCA GTG AAC ATC ATG GAG CTC TAC CTC GGG GCC AAG GAA TCA	288
	Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser	
	85 90 95	
60	AAG AGC TTC ACC TTC TAC CGG CGG GAT ATG GGT CTT ACC TCC AGC TTC	336
	Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe	

	100	105	110	
	GAA TCC GCT GCC TAC CCA GGC TGG TTC CTC TGC ACC TCA CCG GAA GCT			384
5	Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala			
	115	120	125	
	GAC CAG CCT GTC AGG CTC ACT CAG ATC CCT GAG GAC CCC GCC TGG GAT			432
	Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp			
10	130	135	140	
	GCT CCC ATC ACA GAC TTC TAC TTT CAG CAG TGT GAC TA			470
	Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp			
	145	150	155	

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala	
	1	5 10 15
30	Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu	
	20	25 30
	His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn	
	35	40 45
35	Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly	
	50	55 60
40	Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys	
	65	70 75 80
	Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser	
	85	90 95
45	Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe	
	100	105 110
	Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala	
	115	120 125
50	Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp	
	130	135 140
	Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp	
55	145	150 155

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs

60

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 10 (B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15	TTC CAG GAA GGG AAC ATA ATG GAA ATG TAC AAC AAA AAG GAA CCT GTA	48
	Phe Gln Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val	
	1 5 10 15	
20	AAA GCC TCT CTC TTC TAT CAC AAG AAG AGT GGT ACA ACC TCT ACA TTT	96
	Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe	
	20 25 30	
25	GAG TCT GCA GCC TTC CCT GGT TGG TTC ATC GCT GTC TGC TCT AAA GGG	144
	Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly	
	35 40 45	
30	AGC TGC CCA CTC ATT CTG ACC CAA GAA CTG GGG GAA ATC TTC ATC ACT	192
	Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr	
	50 55 60	
35	GAC TTC GAG ATG ATT GTG GTA CAT TAA	219
	Asp Phe Glu Met Ile Val Val His	
	65 70	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids
 40 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	Phe Gln Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val
	1 5 10 15
50	Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe
	20 25 30
	Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly
	35 40 45
55	Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr
	50 55 60
60	Asp Phe Glu Met Ile Val Val His
	65 70

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 809 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

15 (A) NAME/KEY: CDS

(B) LOCATION: 90..569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

20	GAATTCGGCA CGAGTGTAGT GTGCAGACAC ATTCCTTATT CAATCAGGGT CAATCTGCAG	60
	ATTGGCAGCT CAGGAACAAC ATCACCATA ATG AAT AAG GAG AAA GAA CTA AGA	113
	Met Asn Lys Glu Lys Glu Leu Arg	
	1 5	
25	GCA GCA TCA CCT TCG CTT AGA CAT GTT CAG GAT CTT AGT AGT CGT GTG	161
	Ala Ala Ser Pro Ser Leu Arg His Val Gln Asp Leu Ser Ser Arg Val	
	10 15 20	
30	TGG ATC CTG CAG AAC AAT ATC CTC ACT GCA GTC CCA AGG AAA GAG CAA	209
	Trp Ile Leu Gln Asn Asn Ile Leu Thr Ala Val Pro Arg Lys Glu Gln	
	25 30 35 40	
35	ACA GTT CCA GTC ACT ATT ACC TTG CTC CCA TGC CAA TAT CTG GAC ACT	257
	Thr Val Pro Val Thr Ile Thr Leu Leu Pro Cys Gln Tyr Leu Asp Thr	
	45 50 55	
	CTT GAG ACG AAC AGG GGG GAT CCC ACG TAC ATG GGA GTG CAA AGG CCG	305
40	Leu Glu Thr Asn Arg Gly Asp Pro Thr Tyr Met Gly Val Gln Arg Pro	
	60 65 70	
	ATG AGC TGC CTG TTC TGC ACA AAG GAT GGG GAG CAG CCT GTG CTA CAG	353
	Met Ser Cys Leu Phe Cys Thr Lys Asp Gly Glu Gln Pro Val Leu Gln	
	75 80 85	
45	CTT GGG GAA GGG AAC ATA ATG GAA ATG TAC AAC AAA AAG GAA CCT GTA	401
	Leu Gly Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val	
	90 95 100	
50	AAA GCC TCT CTC TTC TAT CAC AAG AAG AGT GGT ACA ACC TCT ACA TTT	449
	Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe	
	105 110 115 120	
55	GAG TCT GCA GCC TTC CCT GGT TGG TTC ATC GCT GTC TGC TCT AAA GGG	497
	Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly	
	125 130 135	
	AGC TGC CCA CTC ATT CTG ACC CAA GAA CTG GGG GAA ATC TTC ATC ACT	545
60	Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr	
	140 145 150	

GAC TTC GAG ATG ATT GTG GTA CAT TAAGGTTTTT AGACACATTG CTCTGTGGCA 599
Asp Phe Glu Met Ile Val Val His
155 160

5

CTCTCTCAAG ATTTCTTGGA TTCTAACAAG AAGCAATCAA AGACACCCCT AACAAAATGG 659

AAGACTGAAA AGAAAAGCTGA GCCCTCCCTG GGCTGTTTTT CCTTGGTGGT GAATCAGATG 719

10 CAGAACATCT TACCATGTTT TCATCCAAAG CATTTACTGT TGGTTTTTAC AAGGAGTGAA 779

TTTTTTAAAA TAAAATCATT TATCTCATAA 809

15 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

25

Met Asn Lys Glu Lys Glu Leu Arg Ala Ala Ser Pro Ser Leu Arg His
1 5 10 15

30

Val Gln Asp Leu Ser Ser Arg Val Trp Ile Leu Gln Asn Asn Ile Leu
20 25 30

Thr Ala Val Pro Arg Lys Glu Gln Thr Val Pro Val Thr Ile Thr Leu
35 40 45

35

Leu Pro Cys Gln Tyr Leu Asp Thr Leu Glu Thr Asn Arg Gly Asp Pro
50 55 60

40

Thr Tyr Met Gly Val Gln Arg Pro Met Ser Cys Leu Phe Cys Thr Lys
65 70 75 80

Asp Gly Glu Gln Pro Val Leu Gln Leu Gly Glu Gly Asn Ile Met Glu
85 90 95

45

Met Tyr Asn Lys Lys Glu Pro Val Lys Ala Ser Leu Phe Tyr His Lys
100 105 110

Lys Ser Gly Thr Thr Ser Thr Phe Glu Ser Ala Ala Phe Pro Gly Trp
115 120 125

50

Phe Ile Ala Val Cys Ser Lys Gly Ser Cys Pro Leu Ile Leu Thr Gln
130 135 140

55

Glu Leu Gly Glu Ile Phe Ile Thr Asp Phe Glu Met Ile Val Val His
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 177 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu
1 5 10 15
Phe Leu Phe His Ser Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser
20 25 30
Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe
35 40 45
Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn
50 55 60
Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro Ile Glu Pro His Ala
65 70 75 80
Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser Cys Val Lys
85 90 95
Ser Gly Asp Glu Thr Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp
100 105 110
Leu Ser Glu Asn Arg Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser
115 120 125
Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp
130 135 140
Phe Leu Cys Thr Ala Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn
145 150 155 160
Met Pro Asp Glu Gly Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp
165 170 175
45 Glu

(2) INFORMATION FOR SEQ ID NO:8:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
1 5 10 15

Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
20 25 30

10 Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
35 40 45

Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
50 55 60

15 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
65 70 75 80

Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met
85 90 95

20 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys
100 105 110

Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile
115 120 125

25 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
130 135 140

30 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
145 150 155 160

Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys
165 170 175

35 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu
180 185 190

40 Asp

(2) INFORMATION FOR SEQ ID NO:9:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: peptide

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Ala Met Ser Glu Asp Ser Cys Val Asn Phe Lys Glu Met Met
1 5 10 15

60 Phe Ile Asp Asn Thr Leu Tyr Phe Ile Pro Glu Glu Asn Gly Asp Leu

	20	25	30
	Glu Ser Asp Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg		
	35	40	45
5	Asn Ile Asn Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe		
	50	55	60
10	Glu Asp Met Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg		
	65	70	75
	Leu Ile Ile Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val		
	85	90	95
15	Thr Leu Ser Val Lys Asp Ser Lys Met Ser Thr Leu Ser Cys Lys Asn		
	100	105	110
	Lys Ile Ile Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp		
	115	120	125
20	Ile Gln Ser Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn		
	130	135	140
25	Lys Met Glu Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys		
	145	150	155
	Gln Lys Glu Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu		
	165	170	175
30	Asn Gly Asp Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser		
	180	185	190

(2) INFORMATION FOR SEQ ID NO:10:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: peptide

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

50	Met Ala Glu Val Pro Lys Leu Ala Ser Glu Met Met Ala Tyr Tyr Ser		
	1	5	10
	Gly Asn Glu Asp Asp Leu Phe Phe Glu Ala Asp Gly Pro Lys Gln Met		
	20	25	30
55	Lys Cys Ser Phe Gln Asp Leu Asp Leu Cys Pro Leu Asp Gly Gly Ile		
	35	40	45
60	Gln Leu Arg Ile Ser Asp His His Tyr Ser Lys Gly Phe Arg Gln Ala		
	50	55	60

Ala Ser Val Val Val Ala Met Asp Lys Leu Arg Lys Met Leu Val Pro
 65 70 75 80
 5 Cys Pro Gln Thr Phe Gln Glu Asn Asp Leu Ser Thr Phe Phe Pro Phe
 85 90 95
 Ile Phe Glu Glu Glu Pro Ile Phe Phe Asp Thr Trp Asp Asn Glu Ala
 100 105 110
 10 Tyr Val His Asp Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp
 115 120 125
 Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala
 130 135 140
 15 Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met
 145 150 155 160
 Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu
 165 170 175
 20 Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp
 180 185 190
 25 Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys
 195 200 205
 Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn
 210 215 220
 30 Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr
 225 230 235 240
 35 Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly
 245 250 255
 Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser Ser
 260 265

40 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
 (B) TYPE: amino acid
 45 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

55 Met Ala Lys Val Pro Asp Met Phe Glu Asp Leu Lys Asn Cys Tyr Ser
 1 5 10 15
 Glu Asn Glu Glu Asp Ser Ser Ser Ile Asp His Leu Ser Leu Asn Gln
 20 25 30
 60

Lys Ser Phe Tyr His Val Ser Tyr Gly Pro Leu His Glu Gly Cys Met
 35 40 45
 5 Asp Gln Ser Val Ser Leu Ser Ile Ser Glu Thr Ser Lys Thr Ser Lys
 50 55 60
 Leu Thr Phe Lys Glu Ser Met Val Val Val Ala Thr Asn Gly Lys Val
 65 70 75 80
 10 Leu Lys Lys Arg Arg Leu Ser Leu Ser Gln Ser Ile Thr Asp Asp Asp
 85 90 95
 Leu Glu Ala Ile Ala Asn Asp Ser Glu Glu Glu Ile Ile Lys Pro Arg
 100 105 110
 15 Ser Ala Pro Phe Ser Phe Leu Ser Asn Val Lys Tyr Asn Phe Met Arg
 115 120 125
 20 Ile Ile Lys Tyr Glu Phe Ile Leu Asn Asp Ala Leu Asn Gln Ser Ile
 130 135 140
 Ile Arg Ala Asn Asp Gln Tyr Leu Thr Ala Ala Ala Leu His Asn Leu
 145 150 155 160
 25 Asp Glu Ala Val Lys Phe Asp Met Gly Ala Tyr Lys Ser Ser Lys Asp
 165 170 175
 Asp Ala Lys Ile Thr Val Ile Leu Arg Ile Ser Lys Thr Gln Leu Tyr
 180 185 190
 30 Val Thr Ala Gln Asp Glu Asp Gln Pro Val Leu Leu Lys Glu Met Pro
 195 200 205
 35 Glu Ile Pro Lys Thr Ile Thr Gly Ser Glu Thr Asn Leu Leu Phe Phe
 210 215 220
 Trp Glu Thr His Gly Thr Lys Asn Tyr Phe Thr Ser Val Ala His Pro
 225 230 235 240
 40 Asn Leu Phe Ile Ala Thr Lys Gln Asp Tyr Trp Val Cys Leu Ala Gly
 245 250 255
 Gly Pro Pro Ser Ile Thr Asp Phe Gln Ile Leu Glu Asn Gln Ala
 260 265 270

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..504

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 144

(D) OTHER INFORMATION: /note= "nucleotide 144 designated

5 G, may be G or T"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 451

(D) OTHER INFORMATION: /note= "nucleotide 451 designated

10 (D) OTHER
C, may be C or T"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 469

(D) OTHER INFORMATION: /note= "nucleotide 469 designated

15 (B) LOCATION: 46
(D) OTHER INFORM
C, may be A, C, G, or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

25	ATG Met 1	AGA Arg	GGC Gly	ACT Thr	CCA Pro 5	GGA Gly	GAC Asp	GCT Ala	GAT Asp	GGT Gly 10	GGA Gly	GGA Gly	AGG Arg	GCC Ala	GTC Val 15	TAT Tyr	48
30	CAA Gln	TCA Ser	ATG Met	TGT Cys 20	AAA Lys	CCT Pro	ATT Ile	ACT Thr	GGG Gly 25	ACT Thr	ATT Ile	AAT Asn	GAT Asp	TTG Leu 30	AAT Asn	CAG Gln	96
35	CAA Gln	GTG Val	TGG Trp 35	ACC Thr	CTT Leu	CAG Gln	GGT Gly 40	CAG Gln	AAC Asn	CTT Leu	GTG Val	GCA Ala	GTT Val 45	CCA Pro	CGA Arg	AGG Arg	144
40	ACC Thr 50	AGT Ser	GTG Val	ACC Thr	CCA Pro	GTC Val	ACT Thr 55	GTT Val	GCT Ala	GTT Val	ATC Ile	ACA Thr 60	TGC Cys	AAG Lys	TAT Tyr	CCA Pro	192
45	GAG Glu 65	GCT Ala	CTT Leu	GAG Glu	CAA Gln 70	GGC Gly	AGA Arg 75	GGG Gly	GAT Asp	CCC Pro	ATT Ile 75	TAT Tyr	TTG Leu	GGA Gly	ATC Ile 80	CAG Gln	240
50	AAT Asn	CCA Pro	GAA Glu	ATG Met 85	TGT Cys	TTG Leu	TAT Tyr	TGT Cys	GAG Glu	AAG Lys 90	GTT Val	GGA Gly	GAA Glu	CAG Gln 95	CCC Pro	ACA Thr	288
55	TTG Leu	CAG Gln	CTA Leu	AAA Lys 100	GAG Glu	CAG Gln	AAG Lys	ATC Ile	ATG Met 105	GAT Asp	CTG Leu	TAT Tyr	GGC Gly 110	CAA Gln	CCC Pro	GAG Glu	336
60	CCC Pro	GTG Val	AAA Lys 115	CCC Pro	TTC Phe	CTT Leu	TTC Phe	TAC Tyr 120	CGT Arg	GCC Ala	AAG Lys	ACT Thr 125	GGT Gly	AGG Arg	ACC Thr	TCC Ser	384
65	ACC Thr 130	CTT Leu	GAG Glu	TCT Ser	GTG Val	GCC Ala	TTC Phe 135	CCG Pro	GAC Asp	TGG Trp	TTC Phe	ATT Ile 140	GCC Ala	TCC Ser	TCC Ser	AAG Lys	432
70	GGA Gly 145	GAC Asp	CAG Gln	CCC Pro	ATC Ile 150	ATT Ile	CTG Leu	ACT Thr	TCA Ser	GAA Glu 155	CTT Leu	TGG Trp 155	CAG Gln	TCA Ser	TAC Tyr	AAC Asn 160	480

ACT GCC TTT GAA TTA AAT ATT AAT G
Thr Ala Phe Glu Leu Asn Ile Asn
165

505

5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 168 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr
1 5 10 15
20 Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln
20 25 30
25 Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Arg
35 40 45
Thr Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro
50 55 60
30 Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
65 70 75 80
Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr
85 90 95
35 Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu
100 105 110
40 Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser
115 120 125
Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys
130 135 140
45 Gly Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Trp Gln Ser Tyr Asn
145 150 155 160
Thr Ala Phe Glu Leu Asn Ile Asn
165

50

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 1195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 67..573

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

10 CCACGATTCA GTCCCCTGGA CTGTAGATAA AGACCCTTTC TTGCCAGGTG CTGAGACAAC 60
 CACACT ATG AGA GGC ACT CCA GGA GAC GCT GAT GGT GGA GGA AGG GCC 108
 Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala
 1 5 10
 15 GTC TAT CAA TCA ATG TGT AAA CCT ATT ACT GGG ACT ATT AAT GAT TTG 156
 Val Tyr Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu
 15 20 25 30
 20 AAT CAG CAA GTG TGG ACC CTT CAG GGT CAG AAC CTT GTG GCA GTT CCA 204
 Asn Gln Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro
 35 40 45
 25 CGA AGT GAC AGT GTG ACC CCA GTC ACT GTT GCT GTT ATC ACA TGC AAG 252
 Arg Ser Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys
 50 55 60
 30 TAT CCA GAG GCT CTT GAG CAA GGC AGA GGG GAT CCC ATT TAT TTG GGA 300
 Tyr Pro Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly
 65 70 75
 35 ATC CAG AAT CCA GAA ATG TGT TTG TAT TGT GAG AAG GTT GGA GAA CAG 348
 Ile Gln Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln
 80 85 90
 40 CCC ACA TTG CAG CTA AAA GAG CAG AAG ATC ATG GAT CTG TAT GGC CAA 396
 Pro Thr Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln
 95 100 105 110
 45 CCC GAG CCC GTG AAA CCC TTC CTT TTC TAC CGT GCC AAG ACT GGT AGG 444
 Pro Glu Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg
 115 120 125
 50 ACC TCC ACC CTT GAG TCT GTG GCC TTC CCG GAC TGG TTC ATT GCC TCC 492
 Thr Ser Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser
 130 135 140
 55 TCC AAG AGA GAC CAG CCC ATC ATT CTG ACT TCA GAA CTT GGG AAG TCA 540
 Ser Lys Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser
 145 150 155
 60 TAC AAC ACT GCC TTT GAA TTA AAT ATA AAT GAC TGA ACT CAGC CTAGAGGTGG 593
 Tyr Asn Thr Ala Phe Glu Leu Asn Ile Asn Asp
 160 165
 65 CAGCTTGGTC TTTGTCTTAA AGTTTCTGGT TCCCAATGTG TTTTCGTCTA CATTTTCTTA 653
 GTGTCATTTT CACGCTGGTG CTGAGACAGG GGCAAGGCTG CTGTTATCAT CTCATTTTAT 713
 AATGAAGAAG AAGCAATTAC TTCATAGCAA CTGAAGAACA GGATGTGGCC TCAGAAGCAG 773

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GAGAGCTGGG TGGTATAAGG CTGTCCTCTC AAGCTGGTGC TGTGTAGGCC ACAAGGCATC 833
 TGCATGAGTG ACTTTAAGAC TCAAAGACCA AACACTGAGC TTTCTTCTAG GGGTGGGTAT 893
 5 GAAGATGCTT CAGAGCTCAT GCGCGTTACC CACGATGGCA TGACTAGCAC AGAGCTGATC 953
 TCTGTTTCTG TTTTGCTTTA TTCCCTCTTG GGATGATATC ATCCAGTCTT TATATGTTGC 1013
 CAATATACCT CATTTGTGTG AATAGAACCT TCTTAGCATT AAGACCTTGT AAACAAAAAT 1073
 10 AATTCTTGTG TTAAGTTAAA TCATTTTTGT CCTAATTGTA ATGTGTAATC TTAAAGTTAA 1133
 ATAACTTTG TGTATTTATA TAATAATAAA GCTAAACTG ATATAAAAAA AAAAAAAAAA 1193
 15 AA 1195

(2) INFORMATION FOR SEQ ID NO:15:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

30 Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr
 1 5 10 15
 Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln
 20 25 30
 35 Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser
 35 40 45
 Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro
 50 55 60
 40 Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
 65 70 75 80
 Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr
 85 90 95
 Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu
 100 105 110
 50 Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser
 115 120 125
 Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys
 130 135 140
 55 Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn
 145 150 155 160
 Thr Ala Phe Glu Leu Asn Ile Asn Asp
 165
 60

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